

Impact of blending the genomic relationship matrix with different levels of pedigree relationships or the identity matrix on genetic evaluations



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$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} \end{bmatrix}$$

$$\underline{\mathbf{G}^* = (1 - \beta)\mathbf{G} + \beta\mathbf{A}_{22}}$$

- Fits a residual polygenic effect (Liu et al., 2014)
- Larger β used when the markers do not explain all additive genetic variance (Meyer et al., 2018)

$$\underline{\mathbf{G}^* = (1 - \beta)\mathbf{G} + \beta\mathbf{I}}$$

- Blending with \mathbf{I} had higher accuracy than with \mathbf{A}_{22} when nearly all QTL identified (Fragomeni et al., 2017)
- Bias increased with $\beta > 0.001$ (Himmelbauer et al., 2021)



Compare:

- Reliability and inflation of GEBV
- Convergence rate
- Elapsed wall-clock time

when blending **G** with different proportions of **A₂₂** or **I**

and

Introduce a more efficient blending algorithm



Data

- U.S. Holstein dataset provided by CDCB
- Pedigree: 9,730,943
- Stature phenotypes: 10,067,745
- Genotypes: 569,404
 - 60k SNP
- Partial dataset: Phenotypes removed from daughters of bulls with at least 50 daughters with records in 2014

Analyses

- BLUP90IOD2OMP1
- $GEBV_{w_x}$, $GEBV_{p_x}$
 - x = blending combination
- APY: 15,000 genotyped animals randomly chosen as core

Current BLUPF90
default

Blending Combinations

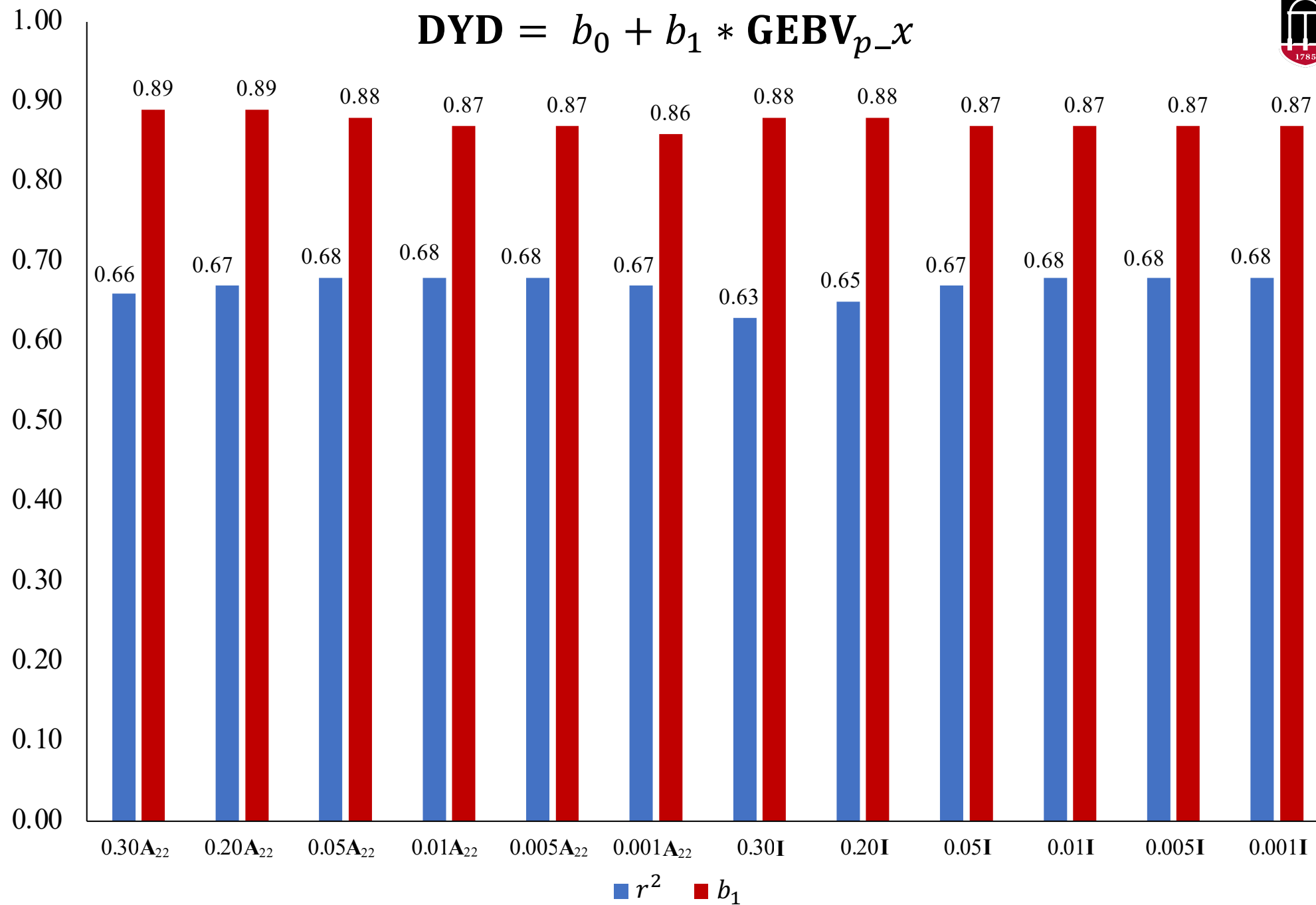
- | | |
|-----------------|------------|
| • $0.30A_{22}$ | • $0.30I$ |
| • $0.20A_{22}$ | • $0.20I$ |
| • $0.05A_{22}$ | • $0.05I$ |
| • $0.01A_{22}$ | • $0.01I$ |
| • $0.005A_{22}$ | • $0.005I$ |
| • $0.001A_{22}$ | • $0.001I$ |

Validation

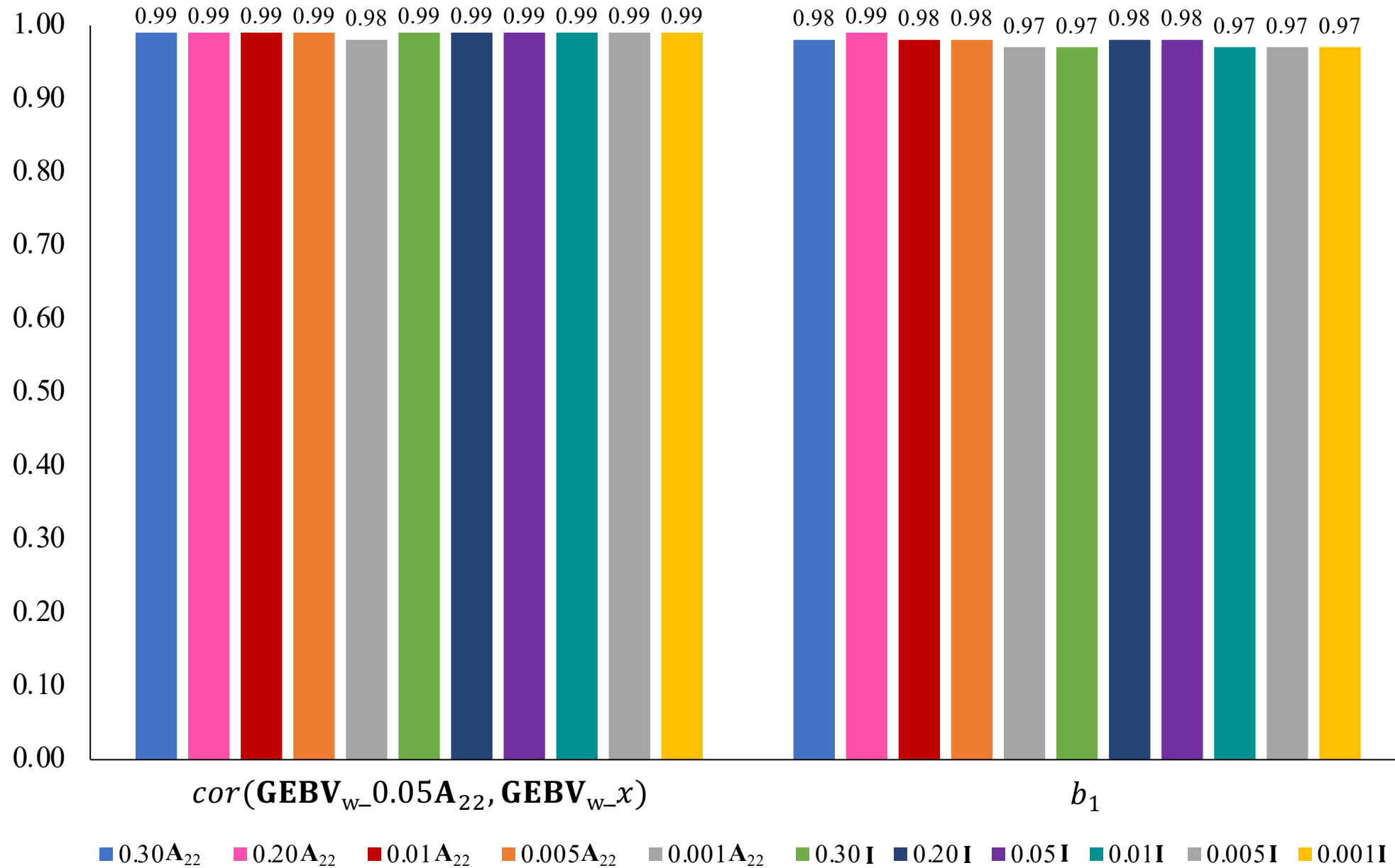
- $DYD = b_0 + b_1 * GEBV_{p_x}$
- $GEBV_{w_0.05A_{22}} = b_0 + b_1 * GEBV_{w_x}$



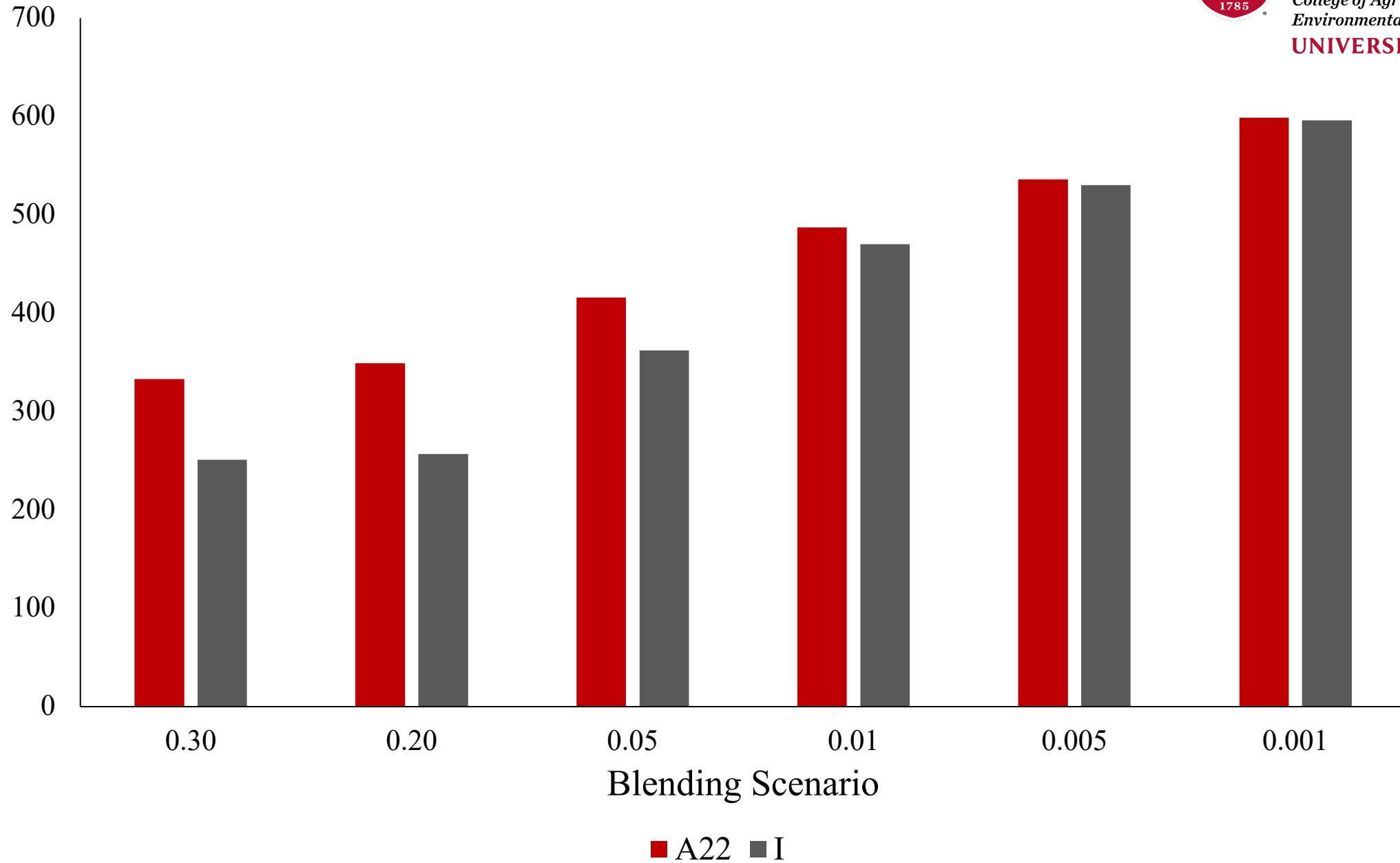
$$DYD = b_0 + b_1 * GEBV_{p-x}$$



$$\text{GEBV}_{w-0.05A_{22}} = b_0 + b_1 * \text{GEBV}_{w-x}$$

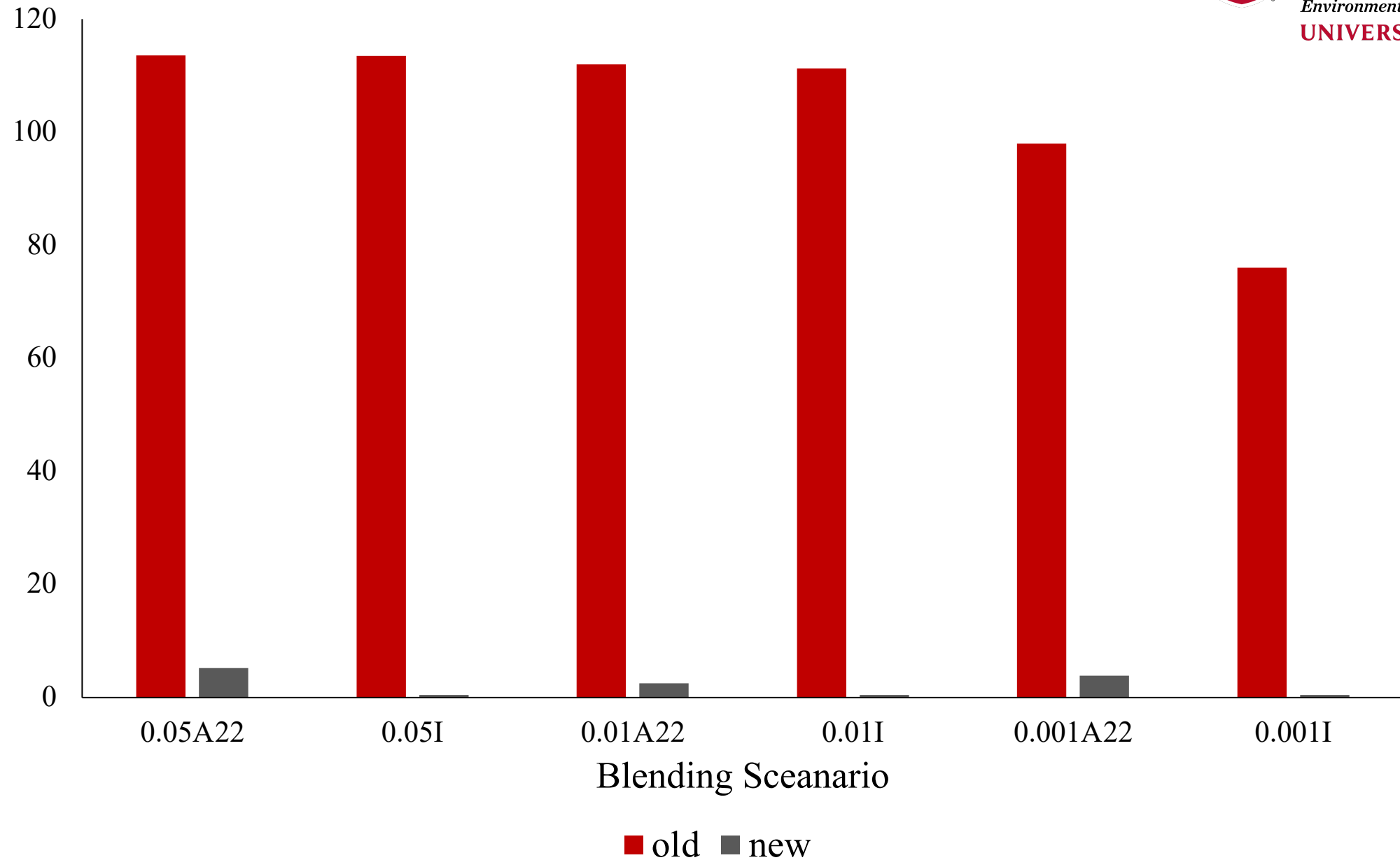


Number of Rounds to Convergence





Elapsed wall-clock time (in minutes)





- Time difference between blending with \mathbf{A}_{22} or \mathbf{I} is not computationally critical
- Blending with a small proportion of \mathbf{I} is enough to maintain accuracy and inflation as with a small proportion of \mathbf{A}_{22}
- Either blending matrix is sufficient
- The new blending algorithm can include virtually any number of genotyped animals

Thank You!

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**Elapsed wall-clock time (in minutes)**

β	old A_{22}	old I	new A_{22}	new I
0.30	54.6	62.2	2.4	2.6
0.20	66.0	61.9	2.9	3.0
0.05	113.6	113.5	5.16	0.006
0.01	61.0	111.3	2.47	0.005
0.005	98.7	77.2	2.33	0.003
0.001	98.0	76.0	3.87	0.004



Time comparison between the old and new blending algorithms.

